Chromosome-Centric Human Proteome Report of Chromosome 11 Team

Mina Park[1], Yeseul Park[1], Hea Ji Lee[1], Yeji Yang[1], Jin Young Kim[1,2], Jong Shin Yoo[1,3], Heeyoun Hwang[1,2]

[1]Research Center for Convergence Analysis, Korea Basic Science Institute, Cheongju 29118, Korea,
[2]Critical Diseases Diagnostics Convergence Research Center, Korea Research Institute of Bioscience and Biotechnology, Daejeon 34141, Korea[b]
[3]Graduate School of Analytical Science and Technology, Chungman National University, Daejeon 34134, Korea

As part of the Chromosome-centric Human Proteome Project (C-HPP), we report on the accurate identification of missing proteins (MP), protein variants, protein isoforms, and the characterization of function unannotated proteins (uPE). Here, we introduce the status of MP, protein variants, isoforms, and uPEs based on the latest release of the neXtProt database (April 2023). According to the neXtProt database, the number of missing proteins in chromosome 11 shows a decreasing pattern. The development of genomic and transcriptomic sequencing techniques has led to a significant increase in the number of protein variants in chromosome 11. In the Protein Atlas, we noticed a decline in uPE1 levels from 2020 to 2023. We observed a notably elevated tissue-specific transcript expression of C11or52 in the kidney. As for uPE1 on chromosome 11, we have studied the functional annotation of CCDC90B (NX_Q9GZT6), SMAP (NX_O00193), and C11orf52 (NX_Q96A22). In addition, we observed changes in protein entries again, where some proteins disappeared, and new proteins were added. Therefore, we always need to use the latest database of neXtProt.